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SEQUENCE LISTING

- <110> Genentech, Inc.
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Godowski, Paul J.
Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
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Williams, P. Mickey
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
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- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20594
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- <150> PCT/US99/20944
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<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
          85              90              95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130              135              140

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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

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aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccgaggga 240

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<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

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Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
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Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
                20                      25                      30

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
    35                      40                      45

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Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
    50                      55                      60

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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

```

65	70	75	80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln	85	90	95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly	100	105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro	115	120	125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln	130	135	140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu	145	150	155
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr	165	170	175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys	180	185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His	195	200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys	210	215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn	225	230	235
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys	245	250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln	260	265	270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys	275	280	285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu	290	295	300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys	305	310	315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His	325	330	335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala	340	345	350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 7

taagtccggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc

49

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
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<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly
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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
 20             25             30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
 35             40             45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
 50             55             60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65             70             75             80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
 85             90             95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
100             105             110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
115             120             125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
130             135             140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
145             150             155             160

His Asp Pro Gly

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<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

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 <223> a, t, c or g

<220>
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 <223> a, t, c or g

<220>
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 <223> a, t, c or g

<220>
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 <222> (188)
 <223> a, t, c or g

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<210> 14
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc 24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15

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<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
          20           25           30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
          35           40           45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
          50           55           60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65           70           75           80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85           90           95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
          100          105          110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
          115          120          125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
          130          135          140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
          145          150          155          160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
          165          170          175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

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 Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45
 Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60
 Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80
 Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95
 Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110
 Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125
 Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140
 Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160
 Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175
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 180 185 190
 Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gcca 24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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 <222> (21)
 <223> a, t, c or g

<400> 26
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<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

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 ctttttttctt gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
                20                      25                      30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
                35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
                50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
                65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
                100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
                115                      120                      125

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Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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			20					25					30			
Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu	
		35					40					45				
Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser	
	50					55					60					
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile	
	65				70					75				80		
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val	
			85						90					95		
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys	
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His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu	
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			180					185					190			
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly	
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	210					215					220					
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His	

225 230 235 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
 245 250 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
 260 265 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
 275 280 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
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Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
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Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
 325 330 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
 340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn
 355 360 365

Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
370 375 380

Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
385 390 395 400

Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
 405 410 415

Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
 420 425 430

Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
 435 440 445

Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
450 455 460

Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
465 470 475 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
 485 490 495

His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
 500 505 510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
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 Arg Tyr Arg
 915

<210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35
 gtgaccctgg ttgtgaatac tcc

23

<210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36
 acagccatgg tctatagctt gg

22

<210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgttc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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ttgtatgaa aaa 1813

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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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20	Ser	Ala	Leu
	25	Pro	Pro
		Ser	Arg
		Ala	Gln
		Leu	Gln
		30	
Leu	His	Leu	Pro
35	Ala	Asn	Arg
	40	Leu	Gln
		Ala	Val
		Glu	Gly
		45	Glu
			Val
Val	Leu	Pro	Ala
50	Trp	Tyr	Thr
	55	Leu	His
		Gly	Glu
		Val	Ser
		60	Ser
			Gln
Pro	Trp	Glu	Val
65	Pro	Phe	Val
	70	Met	Trp
		Phe	Phe
		75	Lys
			Gln
			Lys
			Glu
			Lys
			80
Glu	Asp	Gln	Val
	85	Leu	Ser
		Tyr	Ile
		Asn	Gly
		90	Val
			Thr
			Thr
			Ser
			Lys
			Pro
			95
Gly	Val	Ser	Leu
	100	Val	Tyr
		Ser	Met
		Pro	Ser
		Arg	Asn
		Leu	Ser
		110	Leu
			Arg
Leu	Glu	Gly	Leu
115	Gln	Glu	Lys
	120	Asp	Ser
		Gly	Pro
		Tyr	Ser
		125	Cys
			Ser
			Val
Asn	Val	Gln	Asp
130	Lys	Gln	Gly
	135	Lys	Ser
		Arg	Gly
		His	Ser
		140	Ile
			Lys
			Thr
Leu	Glu	Leu	Asn
145	Val	Leu	Val
	150	Pro	Pro
		Ala	Pro
		155	Pro
			Ser
			Cys
			Arg
			Leu
			160
Gln	Gly	Val	Pro
	165	His	Val
		Gly	Ala
		Asn	Val
		170	Thr
			Leu
			Ser
			Cys
			Gln
			175
Pro	Arg	Ser	Lys
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		Val	Gln
		Tyr	Gln
		185	Trp
			Asp
			Arg
			Gln
			Leu
			Pro
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Ser	Phe	Gln	Thr
	195	Phe	Phe
		Ala	Pro
		Ala	Leu
		200	Asp
			Val
			Ile
			Arg
			Gly
			Ser
			205
Leu	Ser	Leu	Thr
210	Asn	Leu	Ser
	215	Ser	Ser
		Met	Ala
			Gly
			Val
			Tyr
			Val
			Cys
			220
Lys	Ala	His	Asn
225	Glu	Val	Gly
	230	Thr	Ala
		Gln	Cys
		235	Asn
			Val
			Thr
			Leu
			Glu
			240
Val	Ser	Thr	Gly
	245	Pro	Gly
		Ala	Ala
		Val	Val
		250	Ala
			Gly
			Ala
			Val
			Val
			Gly
			255
Thr	Leu	Val	Gly
	260	Leu	Gly
		Leu	Leu
		Ala	Gly
		265	Leu
			Val
			Leu
			Leu
			Tyr
			His
			270
Arg	Arg	Gly	Lys
	275	Ala	Leu
		Glu	Glu
		Pro	Ala
		Asn	Asp
		Ile	Lys
			Glu
			Asp
			285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtggggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50

 <210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 43
 gtgtgacaca gcgtgggc 18

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 44
 gaccggcagg cttctgcg 18

 <210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 45
 cagcagcttc agccaccagg agtgg 25

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 46
 ctgagccgtg ggctgcagtc tcgc 24

 <210> 47

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gtgaaatagc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
 tcacaatttg tgaagatgat aatgaaatgt gaaatttaac tcagtcctgt ggcgaaaatg 240
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
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<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20                      25                      30

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```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35                      40                      45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50                      55                      60

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```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65                      70                      75                      80

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```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85                      90                      95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100                      105                      110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115                      120                      125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130                      135                      140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145                      150                      155                      160

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```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165                      170                      175

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```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val
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Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys
	210					215					220				
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	225					230					235				240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys
				245					250					255	
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met
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Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala
		275					280					285			
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser
	290					295					300				
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln
	305					310					315				320
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile
				325					330					335	
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys
			340					345					350		
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser
		355					360					365			
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp
	370					375					380				
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser
	385					390					395				400
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly
				405					410					415	
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln
			420					425					430		
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr
		435					440					445			
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys
	450					455					460				

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685
 Leu Arg
 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)

<223> a, t, c or g

<400> 50
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 ngaaaagccg gcatatggat tcaaatggca atgttgacgt tgcattttta tattataaga 120
 gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
 aattctgaag aggaggaaa agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
 ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaagggcaca 300
 gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
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 aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaaagat 480
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51
 ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52
 ggagtagaaa gcgcattgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53
 cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

octagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1               5               10               15

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
      20               25               30

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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35               40               45

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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50               55               60

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Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205
 Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60
 atccgccag atggctacaa tgtgta

26

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61
 gcctcccgt ctcctgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtccggt gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240
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 ctttgtctac tatcaacaga ctcttcaagg tgatttttaa aatcgagctg agatgataga 360
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gttgtgaagt 420
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480
 agtggtccca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600
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 ctcttccag aagagtaatt cttcatctaa agccacgaca atgagtgaat atgtgcagtg 960
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300
 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcgttgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
aaataaatga attactcaat ctccatagac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360
tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

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ttacacccag atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggtcttt 660
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
          20                      25                      30

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
  35                      40                      45

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
  50                      55                      60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255
 Thr Val Val

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
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 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590	
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser			
595	600	605	
Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile			
610	615	620	
<210> 74			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 74			
tcacctggag cctttattgg cc			22
<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 75			
ataccagcta taaccaggct gcg			23
<210> 76			
<211> 52			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 76			
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg			50
gg			52
<210> 77			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			

<400> 77
 ccatgtgtct cctcctacaa ag 22

 <210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 78
 gggaatagat gtgatctgat tgg 23

 <210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 79
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 <210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 80
 agcaaccgcc tgaagctcat cc 22

 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 81
 aaggcgcggt gaaagatgta gacg 24

 <210> 82

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 agccaggagg cgggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
 tccctgctgt cgcctgctgc tgggcgcccc gcggggccaa cctctcccag gacgacagcc 240
 agccctggac atctgatgaa acagtgggtg ctgggtggcac cgtgggtgctc aagtgccaaag 300
 tgaaagatca cgaggactca tccctgcaat ggtctaaccg tgctcagcag actctctact 360
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
 cctagcacag tgacgagggga cttggc 26

<210> 88
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 88
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 89
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
 <211> 2755
 <212> DNA
 <213> Homo sapiens

<400> 90
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                      15

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          20                      25                      30

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
          35                      40                      45

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Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
          50                      55                      60

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Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
          65                      70                      75                      80

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Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
          85                      90                      95

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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
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 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
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 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
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 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
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 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
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 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
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 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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675	680	685
Cys Gly Ser His Ser Leu Ser Asp		
690	695	

<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
 gttggatctg ggcaacaata ac 22

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgtgtgac aggcagagtt taag 24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95
 agtcgactgc gtcccctgta cccggcgcca gctgtgttcc tgaccccaga ataaactcagg 60
 gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120
 tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

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gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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ggggcctcag agaatgaggg cggcggttcg cctgtgcctc ctctggcagg cgctctggcc 360
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aatttacatt aaaaaataat ttctaccaaa atggaaagga aatgttctat gttgttcagg 2160
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gttgat 2226

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
 1           5           10          15

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
          20          25          30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35           40           45

```

```

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
 50           55           60

```

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

	340		345		350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala	355	360	365		
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr	370	375	380		
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe	385	390	395	400	
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr	405	410	415		
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln	420	425	430		
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu	435	440	445		
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val	450	455	460		
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu	465	470	475	480	
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala	485	490			

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgccca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 99
 acagagcaga gggcgccttg 20

 <210> 100
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 100
 tcagggacaa gtggtgtctc tccc 24

 <210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 101
 tcagggaagg agtgtgcagt tctg 24

 <210> 102
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 102
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

 <210> 103
 <211> 2026
 <212> DNA
 <213> Homo sapiens

<400> 103

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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgctt 1980
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```

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1             5             10             15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20             25             30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35             40             45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50             55             60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg	Leu Thr Val Val Cys Lys Gln Cys Pro	
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met	Gly Gln Val Gly Glu	
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
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aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctcccagc tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaacac tgctggagggt gtgtgcagca agtcagactt cgagtgccac 420
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tgttcaccac atcccacac ccattgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg	Asp	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu	65	70	75	80
Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly	85	90	95	
Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser	100	105	110	
Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro	115	120	125	
Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro	130	135	140	
Ala	Gly	Thr	Phe	Gly	Pro	Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu	145	150	155	160
Arg	Pro	Cys	Gly	Gly	Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly	165	170	175	
Gly	Ser	Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Gly	Glu	Ala	Cys	180	185	190	
Gly	Gln	Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ala	Ser	His	195	200	205	
Leu	Val	Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Ser	Gly	Pro	210	215	220	
Glu	Glu	Ser	Asn	Cys	Leu	Gln	Cys	Lys	Lys	Gly	Trp	Ala	Leu	His	His	225	230	235	240
Leu	Lys	Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gly	Ala	Asn	Cys	245	250	255	
Gly	Ala	Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg	260	265	270	
Asp	Cys	Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Arg	275	280	285	
Cys	Lys	Lys	Cys	Ser	Pro	Gly	Tyr	Gln	Gln	Val	Gly	Ser	Lys	Cys	Leu	290	295	300	
Asp	Val	Asp	Glu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Gly	Glu	Asn	Lys	Gln	305	310	315	320
Cys	Glu	Asn	Thr	Glu	Gly	Gly	Tyr	Arg	Cys	Ile	Cys	Ala	Glu	Gly	Tyr	325	330	335	
Lys	Gln	Met	Glu	Gly	Ile	Cys	Val	Lys	Glu	Gln	Ile	Pro	Glu	Ser	Ala	340	345	350	

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

```

<400> 113
tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tctccaggg 60
cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
cggggccgccc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
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ggtcgcgttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840
cgaggggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960
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ctcggagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080
ccagggtggtc agcctgccc aatgaggggt gcagaagtgc agctgtgcct cggatggtgc 1140
gtcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200
gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260
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acctaatttt tgcttctcag gaatgagaat ctttgccac tggagagccc ttgctcagtt 1380
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acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
aaagtccctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

```

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

```

<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1             5             10            15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
          20             25            30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
          35             40            45

```

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgcc a taactgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gctgatcgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaa 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgatg ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctccctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggg tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggtcacgtg ggcagccgtc 780
cttgtaaccc tgattctcct ggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtccccgaa gtgaaggaga attcaaacag acctcgatc tccctgggtg agcctggtcg 960
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tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccctcatgc cctccctccc 1140
tttctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgat gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttggt gtggagagca tagtaaat ttagagaact tgaagccaaa aggatttaaa 1620
accgtgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10              15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
          20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
          35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
          50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
          65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85              90              95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125

actcagcagt ggtaggaaaag

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

```

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctgggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgccacccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagcc atgtaccag aaagggcaat gccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct ccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600
tcacctctct caggaatgcc acaaccatgg gggcccctgt gaccctggag agtgccccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggtg gccatgaagg 840
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agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc                                     1210

```

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1              5              10              15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
      20              25              30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
      35              40              45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
      50              55              60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
      65              70              75              80

```

```
<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 128
aagttccagt gccgcaccag tggc

<210> 129
```

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
 cccacgcgtc cgggtctcgtc cgctcgcgca gcgggcggcag cagaggtcgc gcacagatgc 60
 ggggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacccga 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
 ggacccccag cggagggggt ttctttgaag gctctgtagc cegatttcac tgccaagacg 420
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600
 atgaaggatt caagatccgg taccgccgacc tacacaatat ggtttcatta tgtcgcgatg 660
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
 atcgctgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
 ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtagag cgctacaacc 960
 acggaactgt ggtggagttt tactgcatc ctggctacag cctcaccagc gactacaagt 1020
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
 agcaaactgt gccacgacc catgagacc tcctgaccac gtggaagatt gtggcggttca 1140

```

cggaaccag tgtgtgtgtg gtgtgtgtgc tctgtatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc cttcccggag ttccagcagt gaccctgact 1260
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tggaagacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
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cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttggtcc 1620
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gttgatctgt ggagttgatt ctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

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<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1             5             10             15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
 35             40             45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
 50             55             60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
 65             70             75             80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
 100            105            110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
 115            120            125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
 130            135            140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
 145            150            155            160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165            170            175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

180							185					190			
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200				205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
		210					215				220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230				235						240
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245				250					255		
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
			260				265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
		275					280				285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
		290					295				300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310				315						320
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
			325				330					335			
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
			340				345					350			
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
		355					360				365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
		370					375				380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390				395						400
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
			405				410					415			
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
			420				425					430			
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
		435					440				445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
		450					455				460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttataa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtcgcgtc gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120
 ccgtagegcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctctcctcc 900
ttgtgggtcac cacagtgtgta tggtgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080
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tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
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ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgttggt acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1             5             10             15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
                20             25             30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
        35             40             45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
        50             55             60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
        65             70             75             80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
                85             90             95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
        100             105             110

```


Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<210> 138

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaaggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctccctgcagc ctcaaccgcg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctccgcg tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 ccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc ttccaccaac cttcaacca caggaggtct ttattcgttc 660
 cactaacatt ttccggaatc tggagtcacac ccgttgtttg ctggctgggc ttttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcacccctct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaaggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg                                     1514

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<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1             5             10             15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50             55             60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65             70             75             80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100             105             110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115             120             125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130             135             140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145             150             155             160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165             170             175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 143
 ccaactacca aagctgctgg agcc 24

<210> 144
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 144
 gcagctctat taccacggga agga 24

<210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 145
 tccttcccgt ggtaatagag ctgc 24

<210> 146
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 146
 ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<400> 147
 ctctctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
 cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
 ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtc gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcacgtgtgt agaaccaga 480
gagctctttc tccccagtc cagaggggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
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aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttccatgtc 1380
tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgthtctctg aagaactctg aaaaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

```

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
  1             5             10             15

```

```

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
      20             25             30

```

```

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
      35             40             45

```

```

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
      50             55             60

```

```

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
      65             70             75             80

```

```

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
      85             90             95

```

```

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
      100            105            110

```

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149
 ttcagctcat caccttcacc tgcc 24

<210> 150
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 150
 ggctcataca aaataccact aggg 24

<210> 151
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 151
 gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152
 <211> 1427
 <212> DNA
 <213> Homo sapiens

<400> 152
 actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcacctcg 60
 acccacgcgt ccgcggacgc gtgggcggac gcgtgggccg gctaccagga agagtctgcc 120
 gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
 cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagtgtgca gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
 tgctctaacg aaagcactcc tgcctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
 gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840
 ggatggatct aggtatggag ttatggacac caccacagcc caggggccgaa gccctgtgga 900
 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgcct tccttggtctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080


```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1                      5                      10                      15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20                      25                      30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35                      40                      45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50                      55                      60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65                      70                      75                      80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85                      90                      95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
          100                     105                     110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115                     120                     125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130                     135                     140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145                     150                     155                     160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165                     170                     175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180                     185                     190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195                     200                     205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154
ggtgctaaac tgggtgctctg tggc

24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc

20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```

<400> 156
tcatactggtt ccattctcggc acgc                                     24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc       50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgctc cgctgggtggt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcctcggttac tgatcgctctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgctgctg attacaggag ctgggcatgg 240
aattggggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aaggggactgg gtgccaaagg 360
tcataccttt gtggttagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420
gaaggcgaaa attggagatg ttagtatatt agtaaataat gctgggtgtag tctatacatc 480
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gtttcggcag ctggacatgt ctgggtcccc ttcttactgg cttactgttc 660
aagcaagtgt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcggtt cctggcagtt ttaaaacgaa aaatcagtgt 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat ccccatctct tcaatatcat ttttgaggct ttggcagtct 1140
tcatttacta ccacttggtt tttagccaaa agctgattac atatgatata aacagagaaa 1200
taccttttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260
taattttcaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
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gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a aaaaaaaaaa 1771

<210> 159

```

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

```

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
  1               5               10               15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
      20               25               30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
      35               40               45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
      50               55               60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
      65               70               75               80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
      85               90               95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
      100               105               110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
      115               120               125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130               135               140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
      145               150               155               160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
      165               170               175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180               185               190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
      195               200               205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
      210               215               220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
      225               230               235               240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
      245               250               255

```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```
<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence
```

<400> 161
atcccatgca tcagcctggt tacc 24

```
<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 162
gctgggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

```
<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens
```

```
<400> 163
ccacgcgcgc cgcggaacgc tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagggagga gcaccgactg cgcgcacccc tgagagatgg ttggtgccat gtggaaggtg 120
```

```

attgtttcgc tggtcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
caggggtggg cgggagggtt atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttccccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcttg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccaattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
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gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1             5             10            15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20             25            30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35             40            45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50             55            60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65					70						75				80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctggcatc aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

cgagggcctt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
 atttttccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
 tccttgccct tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
 cctggagagc ctgggggagg gctgcctaa caagctttca aaaaacagga gcgacttcca 360
 ctgggctggg ataagacgtg ccggtaggat agggaaagact ggggttagtc ctaatatcaa 420
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
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 cagatgagca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840
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 ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcacgt gcggctctgc 1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct teggctgcac ccgggcccgg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
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acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1             5             10             15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20             25             30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115            120            125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130            135            140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145            150            155            160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165            170            175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450		455		460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr				
465		470		475
				480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly				
	485		490	495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val				
	500		505	510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys				
	515		520	525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln				
	530		535	540
Leu Tyr Phe Leu Gly Glu Gln Arg				
545		550		

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```

<400> 173
ggactcactg gccagggcct tcaatatcac cagccaggac gat 42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g

<400> 174
aggctccccg gcgcggctga gtgcggaactg gagggggaac ccgggtcccc gcgcttagag 60
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120
tgctggctcg cttgggcttc ctgggtgctc gcaggctgga ctggagcacc ctggccctc 180
tgcggtcccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
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cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780
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accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260
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cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgctg 2340
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catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1              5              10              15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20              25              30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35              40              45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50              55              60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65              70              75              80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85              90              95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100             105             110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115             120             125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130             135             140

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Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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ccctggtgag gggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccaggagg cccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaacgcca 240
tggtcccaa gaagctgtcc tgccttcgtt cctgctgct ggcgctcagc ctgacgctac 300
tgctgcccc aagcagacact cggtcgttcg tagtgatag gggtcagac cggtttctcc 360
tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420


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tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttcccttg cgcagtggac tcttggttca 720
aggtcttgct gcccaagata tatccatggc tttatcacaa tgggggcaac atcattagca 780
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ctgtgtcagc tgtaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
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aaacaatcct taccagtggt atgatgttcc ctctgaaaaa tgataacctt gtgaagtggg 1800
ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
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ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggagggtgt accactgcac 2460
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```

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
50 55 60

Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Phe	65	70	75	80
Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln	Pro	Gly	Val	Tyr	Asn	Phe	85	90	95	
Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala	100	105	110	
Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp	115	120	125	
Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His	130	135	140	
Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	145	150	155	160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	165	170	175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	180	185	190	
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	195	200	205	
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	210	215	220	
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	225	230	235	240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	245	250	255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	260	265	270	
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	275	280	285	
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	290	295	300	
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	305	310	315	320
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	325	330	335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile				

			340					345					350			
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	
		355					360					365				
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	
	370					375					380					
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	
385					390					395					400	
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	
				405					410					415		
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	
			420					425					430			
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	
	435						440					445				
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr	
	450					455					460					
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg	
465					470					475					480	
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro	
				485					490					495		
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu	
			500					505					510			
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys	
	515						520					525				
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr	
	530					535					540					
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly	
545					550				555						560	
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr	
			565						570					575		
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu	
			580					585					590			
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu	
	595						600						605			
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu	
	610					615					620					

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggctactcc aagacctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaatc cccttgetca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcaccag aatggtgttg gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120
 gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cctttgaagg 180
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
 ttggtgtggt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt ttgaaccatg 360
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
 tgcactctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
 caaagttagt cattcataat gacggcacta aactcttggg actgaacagc ctttaagaaa 900
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatagct 1200
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
 tgcagcattt gcatatcact ggaacaaaag tggacattct gccaaaacaa ttgtttaaat 1320

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gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
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cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttggtg gaagatcacc 1500
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aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
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ttttcttact aaaaaaaaaa aaaaaaa 1947

```

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100            105            110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115            120            125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130            135            140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145            150            155            160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165            170            175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180            185            190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

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<400> 189
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acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgcctctggg 120
aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctccctctg 180
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```

acattggcat  tgcttagtgg  ttgtgtgggg  agggagacca  cgtgggctca  gtgcttgctt  240
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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	35	40	45	
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	65	70	75	80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	100	105	110	
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	115	120	125	
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	165	170	175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	180	185	190	
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	210	215	220	
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	225	230	235	240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	245	250	255	
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	260	265	270	
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	275	280	285	

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565							570							575		
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe	
580							585							590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr		
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<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctatttc aaactgtggc g 21

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<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>.
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 192
 tttgatgacg attcgaaggt gg 22

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<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc 47

```
<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens
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<400> 194
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ctgctgctgc cgccgcgcgc qtgccectgc cacagcgcca cgcgcttcga cccacactgg 180
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```

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caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
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gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
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taaactcatt gtgcaaatgt aa 2362

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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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```

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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
                20                      25                      30

```

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
  35                      40                      45

```

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe		
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Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys		
	65				70					75					80		
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro		
				85					90					95			
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe		
			100					105					110				
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr		
		115					120					125					
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser		
	130					135					140						
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp		
	145				150					155					160		
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg		
				165					170					175			
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu		
			180					185					190				
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys		
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Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val		
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			260					265					270				
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		275					280					285					
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr		
	290					295					300						
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val		
	305				310					315					320		
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn		
				325					330					335			

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198
 aacttcgagc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199
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<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
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tgtgacaaaa aattaaagca tttagaaaac tt 2372

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100             105             110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115             120             125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130             135             140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 203
 gtcagtgcaca gtacctactc gg 22

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 204
 tggagcagga ggagtagtag tagg 24

<210> 205
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 205
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
 <211> 1620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (973)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (977)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (996)
 <223> a, t, c or g

<220>
 <221> modified_base

<222> (1003)

<223> a, t, c or g

<400> 206

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ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggg aaccctgtgt 180
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accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1              5              10             15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20              25             30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35              40             45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50              55             60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65              70             75             80

```

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285
 Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagtgggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
 cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360
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 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
 tgacgtctcg ctggagatcc aggatctgcy gctggaggac tatgggcgtt accgctgtga 540
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```

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa                                           1985

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<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

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Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                      5                      10                      15

```

```

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
          20                      25                      30

```

```

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
          35                      40                      45

```

```

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
          50                      55                      60

```

```

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
          65                      70                      75                      80

```

```

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
          85                      90                      95

```

```

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
          100                     105                     110

```

```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115					120					125						
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	
130					135					140						
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu	
145					150					155					160	
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg	
165					170					175						
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	
180					185					190						
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	
195					200					205						
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr	
210					215					220						
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro	
225					230					235					240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	
245					250					255						
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu	
260					265					270						
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu	
275					280					285						
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys	
290					295					300						
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	
305					310					315					320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu	
325					330					335						
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr	
340					345					350						
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His									
355					360											

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215

ttcccttgtag ggttgag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217

agccagtgag gaaatgag

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 219
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 gcttctgttg ctactgaggc acggggccca ggggaagcca tcccagacg caggccctca 120
 tggccagggg aggggtgcacc agggggcccc cctgagcgac gctcccatg atgacgcca 180
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
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 cgacgggctgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
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 tgcttggcct ggctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

<400> 226
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tgcagcaggt gcggagcccc 60
 gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
 ccagcctgtc tgcctcgatt tgccgcgcag gcgcctccca gacctagagg ggcgtggcc 240
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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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          20           25           30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
      115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
      130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
      145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
      210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
      225          230          235          240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245          250          255

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Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
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 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
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 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
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 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
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<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233

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24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

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 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
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<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

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<400> 236
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
          20             25             30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
          35             40             45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
          50             55             60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
          65             70             75             80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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 100 105 110
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335
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 340 345 350

<210> 237

<211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 237
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 <210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 238
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 <210> 239
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 239
 gcagagcgga gatgcagcgg cttg 24

 <210> 240
 <211> 18
 <212> DNA
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 240
 ttggcagctt catggagg 18

 <210> 241
 <211> 18
 <212> DNA
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 241
 cctgggcaaa aatgcaac 18

<210> 242
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro
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Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
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Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys			

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Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val					
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Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu					
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Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly					
	470		475		480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr					
	485		490		495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val					
	500		505		510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu					
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Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His					
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Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn					
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr					
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Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr					
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Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala					
	590		595		600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr					
	605		610		615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly					
	620		625		630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly					
	635		640		645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly					
	650		655		660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser					
	665		670		675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
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Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
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Leu Pro Pro Leu Ser Gln Asn Ser
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

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<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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			20						25				30	

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95					100					105				
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
				110					115					120
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
				125					130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
				140					145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
				155					160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp
				230					235					240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu
				245					250					255
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr
				260					265					270
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu
				275					280					285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr
				305					310					315
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr
				320					325					330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser
				335					340					345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn
				350					355					360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
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<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
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Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
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Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
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Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

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Pro Ile Arg Lys	Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp			
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Gly Gly Gln Ala	Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe			
	335	340			345
Met Lys Pro Val	Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly			
	350	355			360
Ile Asn Val Thr	Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp			
	365	370			375
Thr Met Gly Gln	Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu			
	380	385			390
Leu Pro Lys Phe	Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp			
	395	400			405
Pro Lys Ser Leu	Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn			
	410	415			420
Leu Ala Phe Tyr	Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser			
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Asp Gln Gly Asp	Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln			
	440	445			450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tcaggtcgcc	atcataaaca	actctatgtg	caaccacctc	ttcctcaagt	650
acagtttccg	caaggacatc	tttgagaca	tggtttgtgc	tggcaacgcc	700
caaggcggga	aggatgcctg	cttcggtgac	tcaggtggac	ccttggcctg	750
taacaagaat	ggactgtggg	atcagattgg	agtcgtgagc	tggggagtgg	800
gctgtggtcg	gccaatcgg	cccggtgtct	acaccaatat	cagccaccac	850
tttgagtgga	tccagaagct	gatggcccag	agtggcatgt	cccagccaga	900
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tggggccggt	ctgagcctac	ctgagcccat	gcagcctggg	gccactgcc	1000
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

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Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90

Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20					25					30				
Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu
				35					40					45
Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg
				50					55					60
Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln
				65					70					75
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg
				80					85					90
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala
				95					100					105
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu
				110					115					120
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly
				125					130					135
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val
				140					145					150
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro
				155					160					165
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser
				170					175					180
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly
				185					190					195
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn
				200					205					210
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln
				215					220					225
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu
				230					235					240
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala
				245					250					255
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly
				260					265					270
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala
				275					280					285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	20	25	30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
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Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagagggtg ctaagggtg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
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<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
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<220>
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<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
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<220>
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<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
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<220>
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<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggctc 50

<210> 271
<211> 26
<212> DNA
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<220>
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<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agccccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
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<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttgcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga ggggatgct tgtctggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

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gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg cggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggaggagct gcacaacctc taccggggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
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 cagaggtctc aggtccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
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 gcctgcctc cttggatgag gagccagtta ccttccccaa atcgacccat 950
 gttcctatcc caaaatcagc agacaaagt acagacaaaa caaaagtgcc 1000
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 caagggaact cctaccccat gccaggagg aggctgaggc tgaggctgag 1100
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 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	

Lys Thr Glu Arg	Ile Gly Cys Gly Ser	His Phe Cys Glu Lys Leu
	140	145 150
Gln Gly Val Glu	Glu Thr Asn Ile Glu	Leu Leu Val Cys Asn Tyr
	155	160 165
Glu Pro Pro Gly	Asn Val Lys Gly Lys	Arg Pro Tyr Gln Glu Gly
	170	175 180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly	Tyr His Cys Lys Asn Ser
	185	190 195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu	Asp Ala Gln Asp Leu Pro
	200	205 210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe	Arg Ala Thr Glu Ala Ser
	215	220 225
Asp Ser Arg Lys	Met Gly Thr Pro Ser	Ser Leu Ala Thr Gly Ile
	230	235 240
Pro Ala Phe Leu	Val Thr Glu Val Ser	Gly Ser Leu Ala Thr Lys
	245	250 255
Ala Leu Pro Ala	Val Glu Thr Gln Ala	Pro Thr Ser Leu Ala Thr
	260	265 270
Lys Asp Pro Pro	Ser Met Ala Thr Glu	Ala Pro Pro Cys Val Thr
	275	280 285
Thr Glu Val Pro	Ser Ile Leu Ala Ala	His Ser Leu Pro Ser Leu
	290	295 300
Asp Glu Glu Pro	Val Thr Phe Pro Lys	Ser Thr His Val Pro Ile
	305	310 315
Pro Lys Ser Ala	Asp Lys Val Thr Asp	Lys Thr Lys Val Pro Ser
	320	325 330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro	Lys Met Ser Leu Thr Gly
	335	340 345
Ala Arg Glu Leu	Leu Pro His Ala Gln	Glu Glu Ala Glu Ala Glu
	350	355 360
Ala Glu Leu Pro	Pro Ser Ser Glu Val	Leu Ala Ser Val Phe Pro
	365	370 375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln	Ala Thr Leu Asp His Thr
	380	385 390
Gly His Thr Ser	Ser Lys Ser Leu Pro	Asn Phe Pro Asn Thr Ser
	395	400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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tcattctcca agttatggtg gacgtacttc tgttggtctc cctctgcttg 100
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 tttggccaac aactccttg tgttaaagct gaacaggaac cgaatctcag 500
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 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450
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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25					30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu	35	40	45
Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser	50	55	60
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu	65	70	75
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu	80	85	90
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro	95	100	105
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr	110	115	120
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu	125	130	135
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys	140	145	150
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn	155	160	165
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala	170	175	180
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met	185	190	195
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu	200	205	210
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly	215	220	225
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn	230	235	240
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu	245	250	255
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser	260	265	270
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn	275	280	285
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser			

	290		295		300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile	305		310		315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg	320		325		330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala	335		340		345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn	350		355		360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys	365		370		375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys	380		385		390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln	395		400		405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly	410		415		420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	425		430		435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	440		445		450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	455		460		465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	470		475		480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	485		490		495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	500		505		510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	515		520		525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	530		535		540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	545		550		555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	815	820	825
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	830	835	840
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	845	850	855
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	860	865	870
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	875	880	885
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	890	895	900
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	905	910	915
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	920	925	930
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	935	940	945
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu	950	955	960
Asp	Phe	Ser	Ala	Asn	Pro	Glu	Pro	Ala	Ser	Val	Ala	Ser	Ser	Asn	965	970	975
Ser	Phe	Met	Gly	Thr	Phe	Gly	Lys	Ala	Leu	Arg	Arg	Pro	His	Leu	980	985	990
Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Gln	Pro	Ser	Asp	Cys	Gln	Pro	Arg	995	1000	1005
Ala	Phe	Tyr	Leu	Lys	Ala	His	Ser	Ser	Pro	Asp	Leu	Asp	Ser	Gly	1010	1015	1020
Ser	Glu	Glu	Asp	Gly	Lys	Glu	Arg	Thr	Asp	Phe	Gln	Glu	Glu	Asn	1025	1030	1035
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro	1040	1045	1050
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<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly					
	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly					
	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg					
	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp					
	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln					
	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile					
	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val					
	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp					
	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His					
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro					
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Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys					
	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn					
	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val					
	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp					
	410		415		420

Thr Gly Met Tyr	Thr Cys Met Val	Ser Asn Ser Val Gly Asn Thr	
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Thr Ala Ser Ala	Thr Leu Asn Val	Thr Ala Ala Thr Thr Thr Pro	
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Phe Ser Tyr Phe	Ser Thr Val Thr Val	Glu Thr Met Glu Pro Ser	
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Gln Asp Glu Ala	Arg Thr Thr Asp Asn	Asn Val Gly Pro Thr Pro	
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Val Val Asp Trp	Glu Thr Thr Asn Val	Thr Thr Ser Leu Thr Pro	
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Gln Ser Thr Arg	Ser Thr Glu Lys Thr	Phe Thr Ile Pro Val Thr	
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Asp Ile Asn Ser	Gly Ile Pro Gly Ile	Asp Glu Val Met Lys Thr	
	515	520	525
Thr Lys Ile Ile	Ile Gly Cys Phe Val	Ala Ile Thr Leu Met Ala	
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Ala Val Met Leu	Val Ile Phe Tyr Lys	Met Arg Lys Gln His His	
	545	550	555
Arg Gln Asn His	His Ala Pro Thr Arg	Thr Val Glu Ile Ile Asn	
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Val Asp Asp Glu	Ile Thr Gly Asp Thr	Pro Met Glu Ser His Leu	
	575	580	585
Pro Met Pro Ala	Ile Glu His Glu His	Leu Asn His Tyr Asn Ser	
	590	595	600
Tyr Lys Ser Pro	Phe Asn His Thr Thr	Thr Val Asn Thr Ile Asn	
	605	610	615
Ser Ile His Ser	Ser Val His Glu Pro	Leu Leu Ile Arg Met Asn	
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Ser Lys Asp Asn	Val Gln Glu Thr Gln	Ile	
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<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

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Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
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Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
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Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
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Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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	230		235		240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met					
	245		250		255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu					
	260		265		270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly					
	275		280		285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn					
	290		295		300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu					
	305		310		315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser					
	320		325		330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn					
	335		340		345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser					
	350		355		360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile					
	365		370		375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg					
	380		385		390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala					
	395		400		405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn					
	410		415		420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys					
	425		430		435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys					
	440		445		450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln					
	455		460		465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly					
	470		475		480

Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	
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Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	
				500					505					510	
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	
				515					520					525	
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	
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Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	
				545					550					555	
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	
				560					565					570	
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	
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His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	
				590					595					600	
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	
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Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro	
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Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro	
				635					640					645	
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val	
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Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser	
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Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr	
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Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp	
				695					700					705	
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala	
				710					715					720	
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser	
				725					730					735	
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln	
				740					745					750	

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
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Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

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Ser	Phe	Met	Gly	Thr	Phe	Gly	Lys	Ala	Leu	Arg	Arg	Pro	His	Leu
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Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Gln	Pro	Ser	Asp	Cys	Gln	Pro	Arg
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Ser	Glu	Glu	Asp	Gly	Lys	Glu	Arg	Thr	Asp	Phe	Gln	Glu	Glu	Asn
			1085					1090						1095
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro
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<211> 19

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cctaaactga actggacca 19

<210> 297

<211> 19

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<212> DNA

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<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

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<220>
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<400> 312
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<210> 313
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<210> 314
 <211> 3003
 <212> DNA
 <213> Homo Sapien

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<211> 509

<212> PRT

<213> Homo Sapien

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Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
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Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365	370	375
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380	385	390
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395	400	405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
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455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
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<210> 317
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<220>
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<400> 317
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<210> 318
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<210> 319
 <211> 2110
 <212> DNA

<213> Homo Sapien

<400> 319

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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

	320		325		330									
Ala	Gln	Lys	Gly	Lys	Ser	Leu	Ser	Pro	Leu	Ala	Ser	Ile	Thr	Gly
			335						340					345
Ile	Ser	Leu	Phe	Leu	Ile	Ile	Ser	Met	Cys	Leu	Leu	Phe	Leu	Trp
				350					355					360
Lys	Lys	Tyr	Gln	Pro	Tyr	Lys	Val	Ile	Lys	Gln	Lys	Leu	Glu	Gly
				365					370					375
Arg	Pro	Glu	Thr	Glu	Tyr	Arg	Lys	Ala	Gln	Thr	Phe	Ser	Gly	His
				380					385					390
Glu	Asp	Ala	Leu	Asp	Asp	Phe	Gly	Ile	Tyr	Glu	Phe	Val	Ala	Phe
				395					400					405
Pro	Asp	Val	Ser	Gly	Val	Ser	Arg	Ile	Pro	Ser	Arg	Ser	Val	Pro
				410					415					420
Ala	Ser	Asp	Cys	Val	Ser	Gly	Gln	Asp	Leu	His	Ser	Thr	Val	Tyr
				425					430					435
Glu	Val	Ile	Gln	His	Ile	Pro	Ala	Gln	Gln	Gln	Asp	His	Pro	Glu
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<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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 cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
 tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
 ttgcgaaagt agatgtcaca gacgagccag gactgagtgg acggtttatc 300
 ataactgctc ttctactat ttatcattgt aaagatggtg aatttaggcg 350
 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400
 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500
 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600
 ctctgtatga tatttggtgc agattgcctt tgtccttcaa aaaggcgag 650
 accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700
 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750
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acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050
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aaacctttct aaccacttca ttaaaqctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
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Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

	215		220		225
Ser	Glu	Ser	Ala	Gln	Pro
				Leu	Lys
				Lys	Val
				Glu	Glu
				Glu	Gln
				Glu	Glu
				230	240
Ala	Asp	Glu	Glu	Asp	Val
				Ser	Glu
				Glu	Glu
				245	250
				Glu	Ala
				Glu	Ser
				Lys	Glu
				255	
Gly	Thr	Asn	Lys	Asp	Phe
				Pro	Gln
				Asn	Ala
				260	265
				Ile	Arg
				Gln	Arg
				Ser	
				270	
Leu	Gly	Pro	Ser	Leu	Ala
				Thr	Asp
				Lys	Ser
				275	280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttccctcg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

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acttcctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

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agactggcct gcgctggagg acctgtcct gcaggactca gctgcaggtt 500

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gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatc ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
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 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttgtgga 1750
 tcaacagaag ttgactgaca tccttttctg tccttccct tcctggtcct 1800
 tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850
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 gcctgtgcc tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000
 gttagctgtc tagcgcctag caagggtcct ttgtacctca ggtgttttag 2050
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65					70					75

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80					85					90

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110					115					120

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125					130					135

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140					145					150

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155					160					165

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185					190					195

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200					205					210

Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg	215	220	225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His	230	235	240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu	245	250	255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu	260	265	270
Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro	275	280	285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys	290	295	300
Leu	Thr	Pro	Arg	Arg	Gln	Lys	Arg	Leu	Phe	Cys	Arg	Tyr	His	His	305	310	315
Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu	320	325	330
Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met	335	340	345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys	350	355	360
Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr	365	370	375
Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp	380	385	390
Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile	395	400	405
Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn	410	415	420
Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg	425	430	435
Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala	440	445	450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr	455	460	465
Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
 500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
 515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
 530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

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<223> Synthetic Oligonucleotide Probe

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<212> DNA
 <213> Homo Sapien

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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
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Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
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Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
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Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
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Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

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Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr	Phe Thr		
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Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val	Val Ser		
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His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr	Leu Arg		
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His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe	Phe Ile		
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Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala	Ala Leu		
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Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly	Arg Ala		
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Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys	His Gly		
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Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg	Leu Arg		
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala	Arg Pro		
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Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly	Val Gly		
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Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe	Glu Leu		
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Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala	Phe Leu		
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Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu	Met Tyr		
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Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg	Ala Tyr		
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Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu	Thr Val		
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Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val	Gly Leu		
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Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
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Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
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Gly	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr	665	670	675
Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu	680	685	690
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met	695	700	705
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val	710	715	720
Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro	725	730	735
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu	740	745	750
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu	755	760	765
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<400> 340

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<212> PRT

<213> Homo Sapien

<400> 341

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Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
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Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
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Cys Ser Asp Met	Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln				
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Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly					
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<210> 344

<211> 28

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<210> 345

<211> 50

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<400> 347

ccctcatgta ccggctcc 18

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<210> 371

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<223> Synthetic Oligonucleotide Probe

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<400> 372

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<400> 373

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<400> 374

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<400> 375

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<210> 376

<211> 997

<212> DNA

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 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	
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Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	
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Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	
				65					70					75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	
				80					85					90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	
				95					100					105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	
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Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
				125					130					135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	
				140					145					150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	
				155					160					165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	
				170					175					180	

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 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
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<210> 379

<211> 24

<212> DNA

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<223> Synthetic Oligonucleotide Probe

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tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 380

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<211> 26

<212> DNA

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<400> 381

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<210> 382
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ggccttgacg acaaccgt 18

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cacaaactcg aactgcttct g 21

<210> 387

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gggatgtggt gaacacagaa ca 22

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tgccagctgc atgctgccag tt 22

<210> 390

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

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<210> 393

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<223> Synthetic oligonucleotide probe

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<210> 394

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ggcagagact tccagtcact ga 22

<210> 403
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<400> 403
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<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
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<400> 405
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<210> 406
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<400> 406
caggcttaca atgttatgat cagaca 26

<210> 407
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tcaacccttg accctttcct a 21

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ggcaggggac aagccatctc tcct 24

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

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gggccctaac ctcattacct tt 22

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<400> 421
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<210> 422
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 <213> Homo Sapien

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<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
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Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
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Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
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Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
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				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					